



BB-1163 US DIV Correct Sequence Listing

SEQUENCE LISTING

<110> Allen, Stephen M.
Hitz, William D.
Kinney, Anthony J.

<120> Plant Sugar Transport Proteins

<130> BB1163USDIV

<140> 10/051,902

<141> 2002-01-17

<150> 60/083,044

<151> 1998-04-24

<160> 30

<170> Microsoft office 97

<210> 1

<211> 2824

<212> DNA

<213> Zea mays

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<221> unsure

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<222> (622)

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gttaagggaa	cgaacatctg	ctcatgctcc	tcaaacggta	aaaaagagtc	cctcaatggc	2640
aaataggagt	cgtaaagttg	tcaatgtcat	ttaccatatg	ttttacctat	ttgtactgta	2700

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ttataagtca agctattcaa cgctggttgt tgctagaaat ctttagaaca aagatgataa 2760
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Lys Lys Glu Phe Asn Leu Gln Ser Glu Pro Leu Ile Glu Gly Leu Ile
 35 40 45

Val Ala Met Phe Leu Ile Gly Ala Thr Val Ile Thr Thr Ser Pro Gly
 50 55 60

Pro Arg Ala Asp Cys Val Gly Arg Arg Pro Met Leu Val Ala Ser Ala
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65 70 75 80
Val Leu Tyr Phe Val₈₅ Ser Gly Leu Val₉₀ Met Leu Trp Ala Pro Ile₉₅ Val
Tyr Ile Leu Leu₁₀₀ Leu Ala Arg Leu Ile₁₀₅ Asp Gly Phe Gly Ile₁₁₀ Gly Leu
Ala Val Thr₁₁₅ Leu Val Pro Leu Tyr₁₂₀ Ile Ser Glu Thr Ala₁₂₅ Pro His Arg
Xaa Ser₁₃₀ Trp Gly Xaa Xaa Asn₁₃₅ Thr Leu Pro Gln Phe₁₄₀ Ile Gly Val Xaa
Gly₁₄₅ Gly Met Phe Leu Ser₁₅₀ Tyr Cys Met Val Phe₁₅₅ Gly Met Ser Leu Met₁₆₀
Pro Lys Pro Asp Trp₁₆₅ Arg Leu Met Leu Gly₁₇₀ Val Leu Ser Ile Pro₁₇₅ Ser
Leu Xaa Tyr Phe₁₈₀ Gly Leu Thr Val Phe₁₈₅ Tyr Leu Pro Glu Ser₁₉₀ Pro Arg
Trp Leu Val₁₉₅ Ser Lys Gly Arg Met₂₀₀ Ala Glu Ala Lys Arg₂₀₅ Val Xaa Gln
Arg Leu₂₁₀ Arg Gly Arg Glu Asn₂₁₅ Val Ser Xaa Glu Xaa₂₂₀ Ala Leu Leu Val
Glu₂₂₅ Gly Leu Gly Val Gly₂₃₀ Lys Asp Thr Arg Ile₂₃₅ Xaa Glu Tyr Ile Ile₂₄₀
Gly Pro Ala Thr Glu₂₄₅ Ala Ala Asp Asp Leu Val Thr Asp Gly Asp₂₅₅ Lys
Glu Gln Ile Thr₂₆₀ Leu Tyr Gly Pro Glu₂₆₅ Glu Gly Gln Ser Trp₂₇₀ Ile Ala
Arg Pro Ser₂₇₅ Lys Gly Pro Ile Met₂₈₀ Leu Gly Ser Val Leu₂₈₅ Ser Leu Ala
Ser Arg₂₉₀ His Gly Ser Met Val₂₉₅ Asn Gln Ser Val Pro₃₀₀ Leu Met Asp Pro
Ile₃₀₅ Val Thr Leu Phe Gly₃₁₀ Ser Val His Glu Asn₃₁₅ Met Pro Gln Ala Gly₃₂₀
Gly Ser Met Arg Ser₃₂₅ Thr Leu Phe Pro Asn₃₃₀ Phe Gly Ser Met Phe₃₃₅ Ser
Val Thr Asp Gln₃₄₀ His Ala Lys Asn Glu₃₄₅ Gln Trp Asp Glu Glu₃₅₀ Asn Leu
His Arg Asp₃₅₅ Asp Glu Glu Tyr Ala₃₆₀ Ser Asp Gly Ala Gly₃₆₅ Gly Asp Tyr
Glu Asp₃₇₀ Asn Leu His Ser Pro₃₇₅ Leu Leu Ser Arg Gln₃₈₀ Ala Thr Gly Ala
Glu₃₈₅ Gly Lys Asp Ile Val₃₉₀ His His Gly His Arg₃₉₅ Gly Ser Ala Leu Ser₄₀₀
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745

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 <212> DNA
 <213> Oryza sativa

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 tccagattcc cagccgcctc tcttcttggt aggggatccg aaatctcggg ggacgagaga 180
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 atcggcaact tgctgcaggg ctgggataat gcaaccattg cagggtgcggg actgtacatc 300
 aagaagggaat tcaacttgca tagcgacccc cttatcgaag gtctgatcgt ggccatgtcg 360
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 <213> Oryza sativa

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Ser Pro Lys Ser Phe Pro Ile Trp Arg Glu Phe Pro Ile Tyr Leu Pro
 20 25 30

His Leu Gly Val Pro Thr Ser Pro Ser Arg Phe Pro Ala Ala Ser Leu
 35 40 45

Leu Val Arg Gly Ser Glu Ile Ser Val Asp Glu Arg Leu Gly Gly Asn
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50

55

60

Xaa Ser Pro Ala Met Ala Gly Ala Val Leu Val Ala Ile Ala Ala Ser
 65 70 75 80
 Ile Gly Asn Leu Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala
 85 90 95
 Val Leu Tyr Ile Lys Lys Glu Phe Asn Leu His Ser Asp Pro Leu Ile
 100 105 110
 Glu Gly Leu Ile Val Ala Met Ser Leu Ile Gly Ala Thr Ile Ile Thr
 115 120 125
 Thr Xaa Ser
 130

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 <212> DNA
 <213> Oryza sativa

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 <213> Oryza sativa

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 Val Met Gly Phe Gly Pro Ile Pro Asn Ile Leu Cys Ala Glu Ile Phe
 35 40 45
 Pro Thr Thr Val Arg Gly Ile Cys Ile Ala Ile Cys Ala Leu Thr Phe
 50 55 60
 Trp Ile Gly Asp Ile Ile Val Thr Tyr Thr Leu Pro Val Met Leu Asn
 65 70 75 80
 Ala Ile Gly Leu Ala Gly Val Phe Gly Ile Tyr Ala Val Val Cys Ile
 85 90 95

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Leu Ala Phe Leu Phe Val Phe Met Lys Val Pro Glu Thr Lys Gly Met
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Lys Glu Asp
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 <212> DNA
 <213> Glycine max

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 aaaaaaaaaa a a 2601

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 <211> 737
 <212> PRT

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<213> Glycine max

<400> 8

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 35 40 45
 Met Ser Leu Ile Gly Ala Thr Val Ile Thr Thr Cys Ser Gly Pro Ile
 50 55 60
 Ala Asp Trp Leu Gly Arg Arg Pro Met Met Ile Ile Ser Ser Val Leu
 65 70 75 80
 Tyr Phe Leu Gly Gly Leu Val Met Leu Trp Ser Pro Asn Val Tyr Val
 85 90 95
 Leu Cys Leu Ala Arg Leu Leu Asp Gly Phe Gly Ile Gly Leu Ala Val
 100 105 110
 Thr Leu Val Pro Val Tyr Ile Ser Glu Thr Ala Pro Ser Glu Ile Arg
 115 120 125
 Gly Ser Leu Asn Thr Leu Pro Gln Phe Ser Gly Ser Gly Gly Met Phe
 130 135 140
 Leu Ser Tyr Cys Met Val Phe Gly Met Ser Leu Ser Pro Ala Pro Ser
 145 150 155 160
 Trp Arg Leu Met Leu Gly Val Leu Ser Ile Pro Ser Leu Leu Tyr Phe
 165 170 175
 Ala Leu Thr Ile Phe Phe Leu Pro Glu Ser Pro Arg Trp Leu Val Ser
 180 185 190
 Lys Gly Arg Met Leu Glu Ala Lys Lys Val Leu Gln Arg Leu Arg Gly
 195 200 205
 Arg Glu Asp Val Ser Gly Glu Met Ala Leu Leu Val Glu Gly Leu Gly
 210 215 220
 Ile Gly Gly Asp Thr Ser Ile Glu Glu Tyr Ile Ile Gly Pro Ala Asp
 225 230 235 240
 Asp Val Ala Asp Gly His Glu His Ala Thr Glu Lys Asp Lys Ile Arg
 245 250 255
 Leu Tyr Gly Ser Gln Ala Gly Leu Ser Trp Leu Ser Lys Pro Val Thr
 260 265 270
 Gly Gln Ser Ser Ile Gly Leu Ala Ser His His Gly Ser Ile Ile Asn
 275 280 285
 Gln Ser Met Pro Leu Met Asp Pro Leu Val Thr Leu Phe Gly Ser Ile
 290 295 300
 His Glu Lys Leu Pro Glu Thr Gly Ala Arg Gly Ser Met Arg Ser Thr
 305 310 315 320

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Leu Phe Pro Asn Phe Gly Ser Met Phe Ser Thr Ala Glu Pro His Ala
 325 330 335
 Lys Ile Glu Gln Trp Asp Glu Glu Ser Leu Gln Arg Glu Arg Glu Asp
 340 345 350
 Tyr Met Ser Asp Ala Thr Arg Gly Asp Ser Asp Asp Asn Leu His Ser
 355 360 365
 Pro Leu Ile Ser Arg Gln Thr Thr Ser Leu Glu Lys Asp Leu Pro Pro
 370 375 380
 Pro Pro Ser His Gly Ser Ile Leu Gly Ser Met Arg Arg His Ser Ser
 385 390 395 400
 Leu Met Gln Gly Ser Gly Glu Gln Gly Gly Ser Thr Gly Ile Gly Gly
 405 410 415
 Gly Trp Gln Leu Ala Trp Lys Trp Thr Asp Lys Gly Glu Asp Gly Lys
 420 425 430
 Gln Gln Gly Gly Phe Lys Arg Ile Tyr Leu His Glu Glu Gly Val Ser
 435 440 445
 Ala Ser Arg Arg Gly Ser Ile Val Ser Ile Pro Gly Glu Gly Glu Phe
 450 455 460
 Val Gln Ala Ala Ala Leu Val Ser Gln Pro Ala Leu Tyr Ser Lys Glu
 465 470 475 480
 Leu Ile Asp Gly His Pro Val Gly Pro Ala Met Val His Pro Ser Glu
 485 490 495
 Thr Ala Ser Lys Gly Pro Ser Trp Lys Ala Leu Leu Glu Pro Gly Val
 500 505 510
 Lys His Ala Leu Val Val Gly Val Gly Ile Gln Ile Leu Gln Gln Phe
 515 520 525
 Ser Gly Ile Asn Gly Val Leu Tyr Tyr Thr Pro Gln Ile Leu Glu Glu
 530 535 540
 Ala Gly Val Glu Val Leu Leu Ser Asp Ile Gly Ile Gly Ser Glu Ser
 545 550 555 560
 Ala Ser Phe Leu Ile Ser Ala Phe Thr Thr Phe Leu Met Leu Pro Cys
 565 570 575
 Ile Gly Val Ala Met Lys Leu Met Asp Val Ser Gly Arg Arg Gln Leu
 580 585 590
 Leu Leu Thr Thr Ile Pro Val Leu Ile Val Ser Leu Ile Ile Leu Val
 595 600 605
 Ile Gly Ser Leu Val Asn Phe Gly Asn Val Ala His Ala Ala Ile Ser
 610 615 620
 Thr Val Cys Val Val Val Tyr Phe Cys Cys Phe Val Met Gly Tyr Gly
 625 630 635 640
 Pro Ile Pro Asn Ile Leu Cys Ser Glu Ile Phe Pro Thr Arg Val Arg
 645 650 655

BB-1163 US DIV Correct Sequence Listing

Gly Leu Cys Ile Ala Ile Cys Ala Leu Val Phe Trp Ile Gly Asp Ile
660 665 670

Ile Ile Thr Tyr Ser Leu Pro Val Met Leu Gly Ser Leu Gly Leu Gly
675 680 685

Gly Val Phe Ala Ile Tyr Ala Val Val Cys Phe Ile Ser Trp Ile Phe
690 695 700

Val Phe Leu Lys Val Pro Glu Thr Lys Gly Met Pro Leu Glu Val Ile
705 710 715 720

Ser Glu Phe Phe Ser Val Gly Ala Lys Gln Ala Ala Ser Ala Lys Asn
725 730 735

Glu

<210> 9
<211> 1692
<212> DNA
<213> Glycine max

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<213> Glycine max

<400> 10

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BB-1163 US DIV Correct Sequence Listing

Gly Gln Ser Trp Val Ala Arg Pro Val Ala Gly Pro Asn Ser Val Gly
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Pro Leu Val Thr Leu Phe Gly Ser Val His Glu Lys Leu Pro Glu Thr
50 55 60
Gly Ser Thr Leu Phe Pro His Phe Gly Ser Met Phe Ser Val Gly Gly
65 70 75 80
Asn Gln Pro Arg Asn Glu Asp Trp Asp Glu Glu Ser Leu Ala Arg Glu
85 90 95
Gly Asp Asp Tyr Val Ser Asp Ala Gly Asp Ser Asp Asp Asn Leu Gln
100 105 110
Ser Pro Leu Ile Ser Arg Gln Thr Thr Ser Leu Asp Lys Asp Ile Pro
115 120 125
Pro His Ala His Ser Asn Leu Ala Ser Met Arg Gln Gly Ser Leu Leu
130 135 140
His Gly Asn Ser Gly Glu Pro Thr Gly Ser Thr Gly Ile Gly Gly Gly
145 150 155 160
Trp Gln Leu Ala Trp Lys Trp Ser Glu Arg Glu Gly Pro Asp Gly Lys
165 170 175
Lys Glu Gly Gly Phe Lys Arg Ile Tyr Leu His Gln Asp Gly Gly Ser
180 185 190
Gly Ser Arg Arg Gly Ser Val Val Ser Leu Pro Gly Gly Asp Leu Pro
195 200 205
Thr Asp Ser Glu Val Val Gln Ala Ala Ala Leu Val Ser Gln Pro Ala
210 215 220
Leu Tyr Asn Glu Asp Leu Met Arg Gln Arg Pro Val Gly Pro Ala Met
225 230 235 240
Ile His Pro Ser Glu Thr Ile Ala Lys Gly Pro Ser Trp Ser Asp Leu
245 250 255
Phe Glu Pro Gly Val Lys His Ala Leu Ile Val Gly Val Gly Met Gln
260 265 270
Ile Leu Gln Gln Phe Ser Gly Ile Asn Gly Val Leu Tyr Tyr Thr Pro
275 280 285
Gln Ile Leu Glu Gln Ala Gly Val Gly Tyr Leu Leu Ser Ser Leu Gly
290 295 300
Leu Gly Ser Thr Ser Ser Ser Phe Leu Ile Ser Ala Val Thr Thr Leu
305 310 315 320
Leu Met Leu Pro Cys Ile Ala Ile Ala Met Arg Leu Met Asp Ile Ser
325 330 335
Gly Arg Arg Thr Leu Leu Leu Ser Thr Ile Pro Val Leu Ile Ala Ala
340 345 350

BB-1163 US DIV Correct Sequence Listing

Leu Leu Ile Leu Val Leu Gly Ser Leu Val Asp Leu Gly Ser Thr Ala
 355 360 365
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 370 375 380
 Val Met Gly Phe Gly Pro Ile Pro Asn Ile Leu Cys Ala Glu Ile Phe
 385 390 395 400
 Pro Thr Arg Val Arg Gly Leu Cys Ile Ala Ile Cys Ala Leu Thr Phe
 405 410 415
 Trp Ile Cys Asp Ile Ile Val Thr Tyr Thr Leu Pro Val Met Leu Asn
 420 425 430
 Ser Val Gly Leu Ala Gly Val Phe Gly Ile Tyr Ala Val Val Cys Phe
 435 440 445
 Ile Ala Trp Val Phe Val Phe Leu Lys Val Pro Glu Thr Lys Gly Met
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BB-1163 US DIV Correct Sequence Listing

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 <211> 117
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 <213> Triticum aestivum

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 Thr Arg Gly Leu Pro Leu Leu Gly Leu Leu His Leu Ile Ser Leu Val
 35 40 45
 Gly Ser Leu Leu Glu Arg Arg Ser Cys Arg Asp Pro Trp Trp Arg Gly
 50 55 60
 Gly Lys Lys Met Ser Gly Ala Ala Leu Val Ala Ile Ala Ala Ser Ile
 65 70 75 80
 Gly Asn Leu Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala Val
 85 90 95
 Leu Tyr Ile Lys Lys Glu Phe Gln Leu Glu Asn Asn Pro Thr Val Glu
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 Gly Leu Ile Val Ala
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<210> 13
 <211> 1487
 <212> DNA
 <213> Triticum aestivum

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 tgattcatcc attggaggca gtcctccaaag gttcaatctg gaaagatctg tttgaacctg 360
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 taaatggagt tctctactat actcctcaaa ttctggagca agctgggtgtg gctgttcttc 480
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 ttctgctact gggcacaatt cccatcttga tagcatccct aattgttttg ggtgtgggtca 660
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BB-1163 US DIV Correct Sequence Listing

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 <212> PRT
 <213> Triticum aestivum

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 35 40 45
 Ala Asp Ser Arg Arg Gly Ser Val Val Ser Leu Pro Gly Gly Gly Asp
 50 55 60
 Ala Thr Gln Gly Gly Ser Gly Phe Ile His Ala Ala Ala Leu Val Ser
 65 70 75 80
 His Ser Ala Leu Tyr Ser Lys Asp Leu Met Glu Glu Arg Met Ala Ala
 85 90 95
 Gly Pro Ala Met Ile His Pro Leu Glu Ala Ala Pro Lys Gly Ser Ile
 100 105 110
 Trp Lys Asp Leu Phe Glu Pro Gly Val Arg Arg Ala Leu Phe Val Gly
 115 120 125
 Val Gly Ile Gln Met Leu Gln Gln Phe Ala Gly Ile Asn Gly Val Leu
 130 135 140
 Tyr Tyr Thr Pro Gln Ile Leu Glu Gln Ala Gly Val Ala Val Leu Leu
 145 150 155 160
 Ser Asn Leu Gly Leu Ser Ser Ala Ser Ala Ser Ile Leu Ile Ser Ser
 165 170 175
 Leu Thr Thr Leu Leu Met Leu Pro Ser Ile Gly Val Ala Met Arg Leu
 180 185 190
 Met Asp Ile Ser Gly Arg Arg Phe Leu Leu Leu Gly Thr Ile Pro Ile
 195 200 205
 Leu Ile Ala Ser Leu Ile Val Leu Gly Val Val Asn Val Ile Asn Leu
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BB-1163 US DIV Correct Sequence Listing
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<211>      1009
<212>      DNA
<213>      Triticum aestivum
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<211>	228
<212>	PRT
<213>	Triticum aestivum

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BB-1163 US DIV Correct Sequence Listing

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55

60

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85 90 95
Ala Val Leu Val Leu Val Asn Val Leu Asp Val Gly Thr Met Val His
100 105 110
Ala Ala Leu Ser Thr Ile Ser Val Ile Val Tyr Phe Cys Phe Phe Val
115 120 125
Met Gly Phe Gly Pro Ile Pro Asn Ile Leu Cys Ala Glu Ile Phe Pro
130 135 140
Thr Ser Val Arg Gly Ile Cys Ile Ala Ile Cys Ala Leu Thr Phe Trp
145 150 155 160
Ile Gly Asp Ile Ile Val Thr Tyr Thr Leu Pro Val Met Leu Asn Ala
165 170 175
Ile Gly Leu Ala Gly Val Phe Gly Ile Tyr Ala Ile Val Cys Val Leu
180 185 190
Ala Phe Val Phe Val Tyr Met Lys Val Pro Glu Thr Lys Gly Met Pro
195 200 205
Leu Glu Val Ile Thr Glu Phe Phe Ser Val Gly Ala Lys Gln Gly Lys
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Glu Ala Thr Asp
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<210> 17
<211> 615
<212> DNA
<213> Zea mays

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BB-1163 US DIV Correct Sequence Listing

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<211> 167

<212> PRT

<213> Zea mays

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<222> (34)

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<222> (85)

<223> Xaa = any amino acid

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<222> (98)

<223> Xaa = any amino acid

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10

15

BB-1163 US DIV Correct Sequence Listing

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Cys Xaa Ile Leu Ala Ser Met Thr Ser Ile Leu Leu Gly Tyr Asp Ile
35 40 45
Gly Val Met Ser Gly Ala Ser Leu Tyr Ile Lys Lys Asp Leu Lys Ile
50 55 60
Ser Asp Val Lys Leu Glu Ile Leu Met Gly Ile Leu Asn Val Tyr Ser
65 70 75 80
Leu Ile Gly Ser Xaa Ala Ala Gly Arg Thr Ser Asp Trp Ile Gly Arg
85 90 95
Arg Xaa Thr Ile Val Phe Ala Ala Val Ile Phe Phe Ala Gly Ala Xaa
100 105 110
Leu Met Gly Phe Ala Val Asn Tyr Trp Met Leu Met Phe Gly Arg Phe
115 120 125
Val Ala Gly Ile Gly Val Gly Tyr Ala Leu Met Ile Ala Thr Val Tyr
130 135 140
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Pro Glu Val Phe Ile Thr Ser
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<212> DNA
<213> Zea mays

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BB-1163 US DIV Correct Sequence Listing

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aagactgccc tatgagggtg cgtggttcaa ccagagatca ttctgctcct tttcttttcc 1740
cttccttttt cgagtaccat tcccattcgt cgtggtcagt acgatgttgg gtcgttggga 1800
gttagtggtg tcagagtccg cgtgtgcttt gcaagccagg gctgaacca caatcatcag 1860
taacaaaaat tcttcgttt gctttgcaag ccaaaaaaaaa aaaaaaaaaa aaaa 1914

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 <212> PRT
 <213> Zea mays

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 35 40 45
 Ile Lys Lys Asp Leu Asn Ile Thr Asp Val Gln Leu Glu Ile Leu Ile
 50 55 60
 Gly Ile Leu Ser Leu Tyr Ser Leu Phe Gly Ser Phe Ala Gly Ala Arg
 65 70 75 80
 Thr Ser Asp Arg Ile Gly Arg Arg Leu Thr Val Val Phe Ala Ala Val
 85 90 95
 Ile Phe Phe Val Gly Ser Leu Leu Met Gly Phe Ala Val Asn Tyr Gly
 100 105 110
 Met Leu Met Ala Gly Arg Phe Val Ala Gly Val Gly Val Gly Tyr Gly
 115 120 125
 Gly Met Ile Ala Pro Val Tyr Thr Ala Glu Ile Ser Pro Ala Ala Ser
 130 135 140
 Arg Gly Phe Leu Thr Thr Phe Pro Glu Val Phe Ile Asn Ile Gly Ile
 145 150 155 160
 Leu Leu Gly Tyr Leu Ser Asn Phe Ala Phe Ala Arg Leu Pro Leu His
 165 170 175
 Leu Gly Trp Arg Val Met Leu Ala Ile Gly Ala Val Pro Ser Gly Leu
 180 185 190
 Leu Ala Leu Leu Val Phe Cys Met Pro Glu Ser Pro Arg Trp Leu Val
 195 200 205
 Leu Lys Gly Arg Leu Ala Asp Ala Arg Ala Val Leu Glu Lys Thr Ser
 210 215 220
 Ala Thr Pro Glu Glu Ala Ala Glu Arg Leu Ala Asp Ile Lys Ala Ala
 225 230 235 240
 Ala Gly Ile Pro Lys Gly Leu Asp Gly Asp Val Val Thr Val Pro Gly
 245 250 255
 Lys Glu Gln Gly Gly Gly Glu Leu Gln Val Trp Lys Lys Leu Ile Leu
 260 265 270

BB-1163 US DIV Correct Sequence Listing

Ser Pro Thr Pro Ala Val Arg Arg Ile Leu Leu Ser Ala Val Gly Leu
275 280 285
His Phe Phe Gln Gln Ala Ser Gly Ser Asp Ser Val Val Gln Tyr Ser
290 295 300
Ala Arg Leu Phe Lys Ser Ala Gly Ile Thr Asp Asp Asn Lys Leu Leu
305 310 315 320
Gly Val Thr Cys Ala Val Gly Val Thr Lys Thr Phe Phe Ile Leu Val
325 330 335
Ala Thr Phe Leu Leu Asp Arg Ala Gly Arg Arg Pro Leu Leu Leu Ile
340 345 350
Ser Thr Gly Gly Met Ile Val Ser Leu Ile Cys Leu Gly Ser Gly Leu
355 360 365
Thr Val Ala Gly His His Pro Asp Thr Lys Val Ala Trp Ala Val Ala
370 375 380
Leu Cys Ile Ala Ser Thr Leu Ser Tyr Ile Ala Phe Phe Ser Ile Gly
385 390 395 400
Leu Gly Pro Ile Thr Gly Val Tyr Thr Ser Glu Ile Phe Pro Leu Gln
405 410 415
Val Arg Ala Leu Gly Phe Ala Val Gly Val Ala Ser Asn Arg Val Thr
420 425 430
Ser Ala Val Ile Ser Met Thr Phe Leu Ser Leu Ser Lys Ala Ile Thr
435 440 445
Ile Gly Gly Ser Phe Phe Leu Tyr Ser Gly Ile Ala Ala Val Ala Trp
450 455 460
Val Phe Phe Phe Thr Cys Leu Pro Glu Thr Arg Gly Arg Thr Leu Glu
465 470 475 480
Glu Met Gly Lys Leu Phe Gly Met Pro Asp Thr Gly Met Ala Glu Glu
485 490 495
Ala Glu Asp Ala Ala Ala Lys Glu Lys Val Val Glu Leu Pro Ser Ser
500 505 510

Lys

<210> 21
<211> 2017
<212> DNA
<213> Oryza sativa

<400> 21
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ccgtcgcgcc gaagaagaag ggcaacgtcc ggttcgcctt cgcctgcgcc atcctcgctt 180
ccatgacctc catctctctc ggctacgata tcgggggtgat gagcggggcg tcgctgtaca 240
tcaagaagga cttcaacatc agtgacggga aggtggaggt tctcatgggc atactgaacc 300
tctactcgct catcgggtcc ttcgcggcgg ggcggacgtc ggactggatc ggccggcggt 360
acaccatcgt gttcgccgcc gtcataattc tcgcgggggs gttcctcatg gggttcgccg 420
tcaactacgc catgctcatg ttcggccgct tcgtggccgg catcggcgtg ggctacgcgc 480

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tcacgatcgc	gccggtgtac	accgccgagg	tgctgccggc	gtcggcgcg	ggcttcctga	540
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ctttctcccc	cttgccgctg	aacctcgggt	ggcgcatcat	gtcggcgatc	ggcgcgcgcg	660
cgctccgtgct	gctcgcgctc	atggtgctcg	gcacgcccga	gtcggcgcg	tggctggtca	720
tgaagggacg	cctcgcggac	gccaaggtgg	tgctggagaa	gacctccgac	acggcgagg	780
aggccgcgga	gcgccctggc	gacatcaagg	ccgcgcggcg	catccctgag	gagctcgacg	840
gcgacgtggt	gaccgtcccc	aagagaggga	gcggaaacga	gaagcgggtg	tgggaaggagc	900
tcacccctgtc	cccgaacccc	gccatgcggc	gcacccctgt	gtccgggatc	ggcatccact	960
tcttccagca	tgcgttgggc	attcactccg	tcgtcttcta	cagccctctc	gtgttcaaga	1020
gccccggatt	aacgaacgac	aaacacttct	tgggcaccac	ttggccgttc	ggtgtcacca	1080
agaggctttt	catcttgttg	gcgactttct	tcacgcacgg	cgctggcgcg	cggccgctgt	1140
tgctgggacg	cacgggagg	ataatcctct	ccctcatcgg	cctcggcgcc	gggctcaccg	1200
tcgtcggcca	gcaccccac	gccaagatac	cttgggcat	cggcctaagc	atcgccctca	1260
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cggagatctt	cccgcctcag	gtgcgcgcgc	tgggctgtct	gtcggcgctc	gccgccaacc	1380
gcgtcaccag	cggcgctcat	tccatgacct	tcctgtcgct	gtccaaggcc	atcaccatcg	1440
gcggcagctt	cttcctctac	tccggcatcg	ccgcgctcgc	ctgggtgttc	ttctacacct	1500
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ccgccccttc	ggaatcagac	gagccagcca	aggagaagaa	gaagggtgaa	atggccgcca	1620
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tgctgtactg	gctagctagc	aagtagtagc	agcaacgtgg	gaagattcgc	tgatccggcg	1740
ttgtctggaga	gcgacggccg	gcgacgacaa	agcttagctc	cagctcgaga	cttcttaaaa	1800
tcattctcaa	ataccagtat	tttattttgc	tctttgcttt	gtccgtaaaa	gttggtactat	1860
gcgatgaaga	ataccagtat	gtagcaaggc	tgagggtgtg	tgtagctact	agaagtgtca	1920
gtcacgttgt	tcttgaaga	aatgtttaac	tgtaatttaa	gcagtattgt	tgtagtaaat	1980
aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaa			2017

<210> 22
 <211> 510
 <212> PRT
 <213> Oryza sativa

<220>
 <221> UNSURE
 <222> (102)
 <223> Xaa = any amino acid

<400> 22
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 Asn Val Arg Phe Ala Phe Ala Cys Ala Ile Leu Ala Ser Met Thr Ser
 20 25 30
 Ile Leu Leu Gly Tyr Asp Ile Gly Val Met Ser Gly Ala Ser Leu Tyr
 35 40 45
 Ile Lys Lys Asp Phe Asn Ile Ser Asp Gly Lys Val Glu Val Leu Met
 50 55 60
 Gly Ile Leu Asn Leu Tyr Ser Leu Ile Gly Ser Phe Ala Ala Gly Arg
 65 70 75 80
 Thr Ser Asp Trp Ile Gly Arg Arg Tyr Thr Ile Val Phe Ala Ala Val
 85 90 95
 Ile Phe Phe Ala Gly Xaa Phe Leu Met Gly Phe Ala Val Asn Tyr Ala
 100 105 110
 Met Leu Met Phe Gly Arg Phe Val Ala Gly Ile Gly Val Gly Tyr Ala
 115 120 125
 Leu Met Ile Ala Pro Val Tyr Thr Ala Glu Val Ser Pro Ala Ser Ala

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130

135

140

Arg 145	Gly	Phe	Leu	Thr	Ser 150	Phe	Pro	Glu	Val	Phe 155	Ile	Asn	Phe	Gly	Ile 160
Leu	Leu	Gly	Tyr	Val 165	Ser	Asn	Tyr	Ala	Phe 170	Ser	Arg	Leu	Pro	Leu 175	Asn
Leu	Gly	Trp	Arg 180	Ile	Met	Leu	Gly	Ile 185	Gly	Ala	Ala	Pro	Ser 190	Val	Leu
Leu	Ala	Leu 195	Met	Val	Leu	Gly	Met 200	Pro	Glu	Ser	Pro	Arg 205	Trp	Leu	Val
Met	Lys 210	Gly	Arg	Leu	Ala	Asp 215	Ala	Lys	Val	Val	Leu 220	Glu	Lys	Thr	Ser
Asp 225	Thr	Ala	Glu	Glu	Ala 230	Ala	Glu	Arg	Leu	Ala 235	Asp	Ile	Lys	Ala	Ala 240
Ala	Gly	Ile	Pro	Glu 245	Glu	Leu	Asp	Gly	Asp 250	Val	Val	Thr	Val	Pro 255	Lys
Arg	Gly	Ser	Gly 260	Asn	Glu	Lys	Arg	Val 265	Trp	Lys	Glu	Leu	Ile 270	Leu	Ser
Pro	Thr	Pro 275	Ala	Met	Arg	Arg	Ile 280	Leu	Leu	Ser	Gly	Ile 285	Gly	Ile	His
Phe	Phe 290	Gln	His	Ala	Leu	Gly 295	Ile	His	Ser	Val	Val 300	Phe	Tyr	Ser	Pro
Leu 305	Val	Phe	Lys	Ser	Pro 310	Gly	Leu	Thr	Asn	Asp 315	Lys	His	Phe	Leu	Gly 320
Thr	Thr	Trp	Pro	Phe 325	Gly	Val	Thr	Lys	Arg 330	Leu	Phe	Ile	Leu	Leu 335	Ala
Thr	Phe	Phe	Ile 340	Asp	Gly	Val	Gly	Arg 345	Arg	Pro	Leu	Leu	Leu 350	Gly	Ser
Thr	Gly	Gly 355	Ile	Ile	Leu	Ser	Leu 360	Ile	Gly	Leu	Gly	Ala 365	Gly	Leu	Thr
Val	Val 370	Gly	Gln	His	Pro	Asp 375	Ala	Lys	Ile	Pro	Trp 380	Ala	Ile	Gly	Leu
Ser 385	Ile	Ala	Ser	Thr	Leu 390	Ala	Tyr	Val	Ala	Phe 395	Phe	Ser	Ile	Gly	Leu 400
Gly	Pro	Ile	Thr	Trp 405	Val	Tyr	Ser	Ser	Glu 410	Ile	Phe	Pro	Leu	Gln 415	Val
Arg	Ala	Leu	Gly 420	Cys	Ser	Leu	Gly	Val 425	Ala	Ala	Asn	Arg	Val 430	Thr	Ser
Gly	Val	Ile 435	Ser	Met	Thr	Phe	Leu 440	Ser	Leu	Ser	Lys	Ala 445	Ile	Thr	Ile
Gly	Gly 450	Ser	Phe	Phe	Leu	Tyr 455	Ser	Gly	Ile	Ala	Ala 460	Leu	Ala	Trp	Val
Phe	Phe	Tyr	Thr	Tyr	Leu	Pro	Glu	Thr	Arg	Gly	Arg	Thr	Leu	Glu	Glu

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465 470 475 480
 Met Ser Lys Leu Phe Gly Asp Thr Ala Ala Ala Ser Glu Ser Asp Glu
 485 490 495
 Pro Ala Lys Glu Lys Lys Lys Val Glu Met Ala Ala Thr Asn
 500 505 510

<210> 23
 <211> 1853
 <212> DNA
 <213> Glycine max

<400> 23
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 gctagttaga gctgcagaag ctcataagac acttcaggat ttcgatcctc caaagaagcg 240
 caaaaggaac aagtatgctt ttgcttggtc tatgctggcc tccatgactt ccatcttgct 300
 tggttatgat attggagtga tgagtggagc agccatatac ataaaaaggg acctgaaagt 360
 ctgcggacgag caaatcgaga tcctgctcgg aatcatcaac ctatactctc tgataggctc 420
 atgtctcggc ggcagaacct ccgactggat aggtccccgt tacacgattg ttttcgcccg 480
 caccattctc ttgtcggag cacttctcat gggtttctcc cccaattatt cctttctcat 540
 gtttggccgt ttcgtcgtg gcattggcat cggctacgcc ctcatgatag cccccgtcta 600
 caccgccgag gtctccccgg cctcctctcg tggcttcttc acttccttcc ctgaggtatt 660
 tattaatgga gggatattaa ttggatacat atcaaactat gcattttcga agctgacact 720
 aaagggtgga tggcgaatga tgcttgagat tgggtgcaata ccttcggtac tcctaacagt 780
 aggagtgttg gcgatgccgg agtccccaaag gtggcttggt atgagggggtc gtttgggaga 840
 ggcaagaaaa gtgcttaaca aaacctcaga cagcaaggaa gaggcccaac taaggctagc 900
 ggaaatcaaa caagccgcag ggatccccga gagttgcaac gacgacgtcg ttcaggtaaa 960
 taacaacaagc aacgggtgaag gtgtatggaa agagctcttc ctctatccaa cgcccgaat 1020
 tcgtcacatc gtaatcgctg cccttggtat tcacttcttc caacaagcgt cgggcgtaga 1080
 cgccgtcgtt ttgtacagcc ccaggatctt cgaaaaggct gggattacaa acgacacgca 1140
 taagcttctt gcaaccgtgg ccgttggtatt cgtaaagacc gtgttcatct tggcggctac 1200
 gtttacgttg gaccgcgtgg gtcgtcgtcc gttgttattg tctagtgtcg gcggcatggg 1260
 gctctcgctt ctacagcttg cgtacagcct cactgttatt gatcattcgg agaggaaatt 1320
 aatgtgggcc gttggatcga gcatagccat ggtgttggct tacgtggcca cgttctccat 1380
 cgggtgcgggt cccatcacgt ggggtctatag ttctgagatc ttcccgttga ggctgcgggc 1440
 gcarggtgcg gccgcgggag ttgcggtgaa taggaccact agcgcgggtg tctcaatgac 1500
 ttttctgtcc ctactagag ccactactat tgggtggagct ttcttccttt attgtggcat 1560
 tgctactggt ggggtgatat tctttttacac cgtcttgcc gagaccggg gaaaaacgct 1620
 cgaagacatg gaagggtctt ttggtacttt taggtccaaa tccaacgcca gcaaggctgt 1680
 agaaaatgag aatgggcaag tagcacaagt ccagctagga accaatgtcc aaacttgaaa 1740
 aatgagtatt gggacatcca gtaatagtga agtaatttcg tgattttttt tttgtttttt 1800
 acttttttaga ctagtcttcc aaatcaaaac gagaagttaa agtgaaaaaa aaa 1853

<210> 24
 <211> 523
 <212> PRT
 <213> Glycine max

<400> 24
 Met Thr Glu Gly Lys Leu Val Glu Ala Ala Glu Ala His Lys Thr Leu
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 Gln Asp Phe Asp Pro Pro Lys Lys Arg Lys Arg Asn Lys Tyr Ala Phe
 20 25 30
 Ala Cys Ala Met Leu Ala Ser Met Thr Ser Ile Leu Leu Gly Tyr Asp
 35 40 45
 Ile Gly Val Met Ser Gly Ala Ala Ile Tyr Ile Lys Arg Asp Leu Lys
 50 55 60

BB-1163 US DIV Correct Sequence Listing

Val Ser Asp Glu Gln Ile Glu Ile Leu Leu Gly Ile Ile Asn Leu Tyr
 65 70 75 80
 Ser Leu Ile Gly Ser Cys Leu Ala Gly Arg Thr Ser Asp Trp Ile Gly
 85 90 95
 Pro Arg Tyr Thr Ile Val Phe Ala Gly Thr Ile Phe Phe Val Gly Ala
 100 105 110
 Leu Leu Met Gly Phe Ser Pro Asn Tyr Ser Phe Leu Met Phe Gly Arg
 115 120 125
 Phe Val Ala Gly Ile Gly Ile Gly Tyr Ala Leu Met Ile Ala Pro Val
 130 135 140
 Tyr Thr Ala Glu Val Ser Pro Ala Ser Ser Arg Gly Phe Leu Thr Ser
 145 150 155 160
 Phe Pro Glu Val Phe Ile Asn Gly Gly Ile Leu Ile Gly Tyr Ile Ser
 165 170 175
 Asn Tyr Ala Phe Ser Lys Leu Thr Leu Lys Val Gly Trp Arg Met Met
 180 185 190
 Leu Gly Val Gly Ala Ile Pro Ser Val Leu Leu Thr Val Gly Val Leu
 195 200 205
 Ala Met Pro Glu Ser Pro Arg Trp Leu Val Met Arg Gly Arg Leu Gly
 210 215 220
 Glu Ala Arg Lys Val Leu Asn Lys Thr Ser Asp Ser Lys Glu Glu Ala
 225 230 235 240
 Gln Leu Arg Leu Ala Glu Ile Lys Gln Ala Ala Gly Ile Pro Glu Ser
 245 250 255
 Cys Asn Asp Asp Val Val Gln Val Asn Lys Gln Ser Asn Gly Glu Gly
 260 265 270
 Val Trp Lys Glu Leu Phe Leu Tyr Pro Thr Pro Ala Ile Arg His Ile
 275 280 285
 Val Ile Ala Ala Leu Gly Ile His Phe Phe Gln Gln Ala Ser Gly Val
 290 295 300
 Asp Ala Val Val Leu Tyr Ser Pro Arg Ile Phe Glu Lys Ala Gly Ile
 305 310 315 320
 Thr Asn Asp Thr His Lys Leu Leu Ala Thr Val Ala Val Gly Phe Val
 325 330 335
 Lys Thr Val Phe Ile Leu Ala Ala Thr Phe Thr Leu Asp Arg Val Gly
 340 345 350
 Arg Arg Pro Leu Leu Leu Ser Ser Val Gly Gly Met Val Leu Ser Leu
 355 360 365
 Leu Thr Leu Ala Ile Ser Leu Thr Val Ile Asp His Ser Glu Arg Lys
 370 375 380
 Leu Met Trp Ala Val Gly Ser Ser Ile Ala Met Val Leu Ala Tyr Val
 385 390 395 400

BB-1163 US DIV Correct Sequence Listing

Ala Thr Phe Ser Ile Gly Ala Gly Pro Ile Thr Trp Val Tyr Ser Ser
405 410 415

Glu Ile Phe Pro Leu Arg Leu Arg Ala Gln Gly Ala Ala Ala Gly Val
420 425 430

Ala Val Asn Arg Thr Thr Ser Ala Val Val Ser Met Thr Phe Leu Ser
435 440 445

Leu Thr Arg Ala Ile Thr Ile Gly Gly Ala Phe Phe Leu Tyr Cys Gly
450 455 460

Ile Ala Thr Val Gly Trp Ile Phe Phe Tyr Thr Val Leu Pro Glu Thr
465 470 475 480

Arg Gly Lys Thr Leu Glu Asp Met Glu Gly Ser Phe Gly Thr Phe Arg
485 490 495

Ser Lys Ser Asn Ala Ser Lys Ala Val Glu Asn Glu Asn Gly Gln Val
500 505 510

Ala Gln Val Gln Leu Gly Thr Asn Val Gln Thr
515 520

<210> 25
<211> 2089
<212> DNA
<213> Triticum aestivum

<400> 25

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gggcaacgtg	aggttcgcct	tcgcctgcgc	catcctcgcc	tccatgacct	ccatcctcct	180
cggctacgac	atcggcggtga	tgagcggagc	gtcgtgttac	atccagaagg	atctgaagat	240
caacgacacc	cagctggagg	tcctcatggg	catcctcaac	gtgtactcgc	tcatctggctc	300
cttcgcggcg	gggcggacgt	ccgactggat	cggccggcgc	ttcaccatcg	tcttcgccgc	360
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gttcgggcg	ttcgtggccg	gcatcggcgt	ggggtacgct	ctcatgatcg	cgcccgtgaa	480
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gggcatcgac	gccgtcgtgc	tctacagccc	gctagttttc	aagagcgccg	gcatcacggg	1020
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ggtggccacc	ttcctctcgc	accgcattcg	ccggcgggcg	ctgggtgctga	ccagcacggg	1140
cggcatgctc	gtctccttag	tgggcctcgc	gacggggctc	accgtcatca	gccgccaccc	1200
ggacgagaag	atcacctggg	ccatcgtcct	gtgcatcttc	tgcatcatgg	cctacgtggc	1260
cttcttctcc	atcggcctcg	gccccatcac	gtgggtgtac	agctcggaga	tcttcccgtc	1320
gcacgtgcgc	gcgtgggct	gctccctggg	cgtggccgtc	aaccgcctga	ccagcggcgt	1380
gatctccatg	accttcattt	cgctgtccaa	ggccatgacc	atcggcgggc	ccttcttctc	1440
cttcgccggc	atcgccctcat	tcgcatgggt	gttcttcttc	gcctacctgc	cggagacccg	1500
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cgccgcggaa	gccgacgacg	acgccgggga	gaagaagggt	gaaatggccg	ccaccaactg	1620
accgcaagtt	ggcagatcgc	gatgcgaaga	cttgcgctgt	atccgtctcg	gctagctagc	1680
tgccacaagg	ccacatagat	gacgaagtag	cgtgggaaga	ttcgctgatc	cggccggagc	1740
tgccggaggg	cgacggcaag	ctccagctcg	atcgagacgt	taatggcttc	ttaaagtgtc	1800
taagtttaat	gtttcgctct	ttggttttgt	ccgggtaggt	cgtagagcaat	ccggtagtag	1860
cgatgccaa	gctaatacgc	gccggacgga	ctagactact	gtagtagact	gtagaggtgt	1920

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accgttgcta cttccgtggc gtttgtctgc atgattagga gagaaaactg gcggtggttc 1980
gaggactcta cctgccgac gagtgagtca agcgagccac ggaaaatgtg taagaaaaaa 2040
atattaagta tgtgtattgt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2089

<210> 26
<211> 539
<212> PRT
<213> Triticum aestivum

<400> 26
Ala Pro Leu Asn Tyr Thr Gln Gly Gly Pro Arg Arg His Asn Pro Gln
1 5 10 15
Ala Ala Ser Arg Gly Ala Ser Ser Thr Met Asp Arg Ala Ala Leu Pro
20 25 30
Ala Ala Val Glu Pro Lys Lys Lys Gly Asn Val Arg Phe Ala Phe Ala
35 40 45
Cys Ala Ile Leu Ala Ser Met Thr Ser Ile Leu Leu Gly Tyr Asp Ile
50 55 60
Gly Val Met Ser Gly Ala Ser Leu Tyr Ile Gln Lys Asp Leu Lys Ile
65 70 75 80
Asn Asp Thr Gln Leu Glu Val Leu Met Gly Ile Leu Asn Val Tyr Ser
85 90 95
Leu Ile Gly Ser Phe Ala Ala Gly Arg Thr Ser Asp Trp Ile Gly Arg
100 105 110
Arg Phe Thr Ile Val Phe Ala Ala Val Ile Phe Phe Ala Gly Ala Leu
115 120 125
Ile Met Gly Phe Ser Val Asn Tyr Ala Met Leu Met Phe Gly Arg Phe
130 135 140
Val Ala Gly Ile Gly Val Gly Tyr Ala Leu Met Ile Ala Pro Val Asn
145 150 155 160
Thr Gly Glu Val Ser Pro Ala Ser Ala Arg Gly Val Leu Thr Ser Phe
165 170 175
Pro Glu Val Phe Ile Asn Phe Gly Ile Leu Leu Gly Tyr Val Ser Asn
180 185 190
Phe Ala Phe Ala Arg Leu Ser Leu Arg Leu Gly Trp Arg Ile Met Leu
195 200 205
Gly Ile Gly Ala Val Pro Ser Val Leu Leu Ala Phe Met Val Leu Gly
210 215 220
Met Pro Glu Ser Pro Arg Trp Leu Val Met Lys Gly Arg Leu Ala Asp
225 230 235 240
Ala Lys Val Val Leu Ala Lys Thr Ser Asp Thr Pro Glu Glu Ala Ala
245 250 255
Glu Arg Ile Ala Asp Ile Lys Thr Ala Ala Gly Ile Pro Leu Gly Leu
260 265 270
Asp Gly Asp Val Val Pro Val Pro Lys Asn Lys Gly Ser Ser Glu Glu
275 280 285

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Lys Arg Val Leu Lys Asp Leu Ile Leu Ser Pro Thr Ile Ala Met Arg
 290 295 300
 His Ile Leu Ile Ala Gly Ile Gly Ile His Phe Phe Gln Gln Ser Ser
 305 310 315 320
 Gly Ile Asp Ala Val Val Leu Tyr Ser Pro Leu Val Phe Lys Ser Ala
 325 330 335
 Gly Ile Thr Gly Asp Ser Arg Leu Arg Gly Thr Thr Val Ala Val Gly
 340 345 350
 Ala Thr Asn Thr Val Phe Ile Leu Val Ala Thr Phe Leu Leu Asp Arg
 355 360 365
 Ile Arg Arg Arg Pro Leu Val Leu Thr Ser Thr Gly Gly Met Leu Val
 370 375 380
 Ser Leu Val Gly Leu Ala Thr Gly Leu Thr Val Ile Ser Arg His Pro
 385 390 395 400
 Asp Glu Lys Ile Thr Trp Ala Ile Val Leu Cys Ile Phe Cys Ile Met
 405 410 415
 Ala Tyr Val Ala Phe Phe Ser Ile Gly Leu Gly Pro Ile Thr Trp Val
 420 425 430
 Tyr Ser Ser Glu Ile Phe Pro Leu His Val Arg Ala Leu Gly Cys Ser
 435 440 445
 Leu Gly Val Ala Val Asn Arg Leu Thr Ser Gly Val Ile Ser Met Thr
 450 455 460
 Phe Ile Ser Leu Ser Lys Ala Met Thr Ile Gly Gly Ala Phe Phe Leu
 465 470 475 480
 Phe Ala Gly Ile Ala Ser Phe Ala Trp Val Phe Phe Phe Ala Tyr Leu
 485 490 495
 Pro Glu Thr Arg Gly Arg Thr Leu Glu Asp Met Ser Ser Leu Phe Gly
 500 505 510
 Asn Thr Ala Thr His Lys Gln Gly Ala Ala Glu Ala Asp Asp Asp Ala
 515 520 525
 Gly Glu Lys Lys Val Glu Met Ala Ala Thr Asn
 530 535

<210> 27
 <211> 1872
 <212> DNA
 <213> Triticum aestivum

<400> 27
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 gaggacgtcc gactgggtcg gccgcccgcgt caccgtcgtc ttcgcggccg ccattctcaa 420
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cggccaggag aagcagggtg ggaaggagct catcttttcg ccgaccccag ccatgcggtg 960
catactgctc gcggcgctcg gcatccattt ctttcagcag gcgacgggct ccgactccgt 1020
cgtgctctat agcccacgcg tgttcagag cgcgggcatc accggcgaca accacctgct 1080
cggcgccaca tgcgccatgg gggtcatgaa gacgctcttc atcctgggtg ccacgtttca 1140
gctcgaccgc gtcggcaggc ggccgctgct gctgaccagc acggccggca tgctcgcctg 1200
tctcatcggc ctcgggacgg gcctcaccgt cgtgggtcgg caccggagc ccaaggtccc 1260
gtggggccatc ggctgtgca tcgtgtccat cttggcctac gtgtccttct tctccatcgg 1320
cctcggggccc ctacaccagcg tgtacacctc ggaggtcttc ccactgcggg tgcgcgcgct 1380
gggcttcgcg ctgggcacgt catgcaaccg cgtcaccagc gccgcgggtc ccatgtcctt 1440
cctgtccttg tccaaggcca tcaccatcgg cggcagcttc ttcctgtacg ccggcatcgc 1500
ggcgaatagga tggattttct tcttcacctt cattccggag acgcgtggcc tgccgctcga 1560
ggagataggg aagcttttcg gcatgacgga caccggcgtc gaagcccaag acaccgccac 1620
gaaagacaag gcgaaagtag gggagatgaa ctagtgaagt agacgtcaac caactgttac 1680
cgatgtacta ccatagagat gtatctgata aacgtggcaa tataagtgtc acggactctt 1740
ggtgctcatt gatggattgt ttggataaaa tttcaagaga attgtttcaa gtttggatcc 1800
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1860
aaaaaaaaaa aa 1872

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<210> 28
 <211> 529
 <212> PRT
 <213> Triticum aestivum

<400> 28
 Met Lys Met Ser Pro Glu Arg Lys Gly Ala Glu Asp Lys Glu Glu Gly
 1 5 10 15
 Ser Arg Met Ala Ser Ala Ala Leu Pro Glu Pro Gly Ala Val His Pro
 20 25 30
 Arg Asn Lys Gly Asn Phe Lys Tyr Ala Phe Thr Cys Ala Leu Cys Ala
 35 40 45
 Ser Met Ala Thr Ile Val Leu Gly Tyr Asp Val Gly Val Met Ser Gly
 50 55 60
 Ala Ser Leu Tyr Ile Lys Arg Asp Leu Gln Ile Thr Asp Val Gln Leu
 65 70 75 80
 Glu Ile Met Met Gly Ile Leu Ser Val Tyr Ala Leu Ile Gly Ser Phe
 85 90 95
 Leu Gly Ala Arg Thr Ser Asp Trp Val Gly Arg Arg Val Thr Val Val
 100 105 110
 Phe Ala Ala Ala Ile Phe Asn Asn Gly Ser Leu Leu Met Gly Phe Ala
 115 120 125
 Val Asn Tyr Ala Met Leu Met Val Gly Arg Phe Val Thr Gly Ile Gly
 130 135 140
 Val Gly Tyr Ala Ile Met Val Ala Pro Val Tyr Thr Pro Glu Val Ser
 145 150 155 160
 Pro Ala Ser Ala Arg Gly Phe Leu Thr Ser Phe Thr Glu Val Phe Ile
 165 170 175

BB-1163 US DIV Correct Sequence Listing

Asn Val Gly Ile Leu Leu Gly Tyr Val Ser Asn Tyr Ala Phe Ala Arg
 180 185 190
 Leu Pro Leu His Leu Ser Trp Arg Val Met Leu Gly Ile Gly Ala Val
 195 200 205
 Pro Ser Ala Leu Leu Ala Leu Met Val Phe Gly Met Pro Glu Ser Pro
 210 215 220
 Arg Trp Leu Val Met Lys Gly Arg Leu Ala Asp Ala Arg Ala Val Leu
 225 230 235 240
 Ala Lys Thr Ser Asp Thr Pro Glu Glu Ala Val Glu Arg Leu Asp Gln
 245 250 255
 Ile Lys Ala Ala Gly Ile Pro Arg Glu Leu Asp Gly Asp Val Val
 260 265 270
 Val Met Pro Lys Thr Lys Gly Gly Gln Glu Lys Gln Val Trp Lys Glu
 275 280 285
 Leu Ile Phe Ser Pro Thr Pro Ala Met Arg Arg Ile Leu Leu Ala Ala
 290 295 300
 Leu Gly Ile His Phe Phe Gln Gln Ala Thr Gly Ser Asp Ser Val Val
 305 310 315 320
 Leu Tyr Ser Pro Arg Val Phe Gln Ser Ala Gly Ile Thr Gly Asp Asn
 325 330 335
 His Leu Leu Gly Ala Thr Cys Ala Met Gly Val Met Lys Thr Leu Phe
 340 345 350
 Ile Leu Val Ala Thr Phe Gln Leu Asp Arg Val Gly Arg Arg Pro Leu
 355 360 365
 Leu Leu Thr Ser Thr Ala Gly Met Leu Ala Cys Leu Ile Gly Leu Gly
 370 375 380
 Thr Gly Leu Thr Val Val Gly Arg His Pro Asp Ala Lys Val Pro Trp
 385 390 395 400
 Ala Ile Gly Leu Cys Ile Val Ser Ile Leu Ala Tyr Val Ser Phe Phe
 405 410 415
 Ser Ile Gly Leu Gly Pro Leu Thr Ser Val Tyr Thr Ser Glu Val Phe
 420 425 430
 Pro Leu Arg Val Arg Ala Leu Gly Phe Ala Leu Gly Thr Ser Cys Asn
 435 440 445
 Arg Val Thr Ser Ala Ala Val Ser Met Ser Phe Leu Ser Leu Ser Lys
 450 455 460
 Ala Ile Thr Ile Gly Gly Ser Phe Phe Leu Tyr Ala Gly Ile Ala Ala
 465 470 475 480
 Ile Gly Trp Ile Phe Phe Phe Thr Phe Ile Pro Glu Thr Arg Gly Leu
 485 490 495
 Pro Leu Glu Glu Ile Gly Lys Leu Phe Gly Met Thr Asp Thr Ala Val
 500 505 510

BB-1163 US DIV Correct Sequence Listing

Glu Ala Gln Asp Thr Ala Thr Lys Asp Lys Ala Lys Val Gly Glu Met
515 520 525

Asn

<210> 29
<211> 729
<212> PRT
<213> Arabidopsis thaliana

<400> 29
Met Ser Gly Ala Val Leu Val Ala Ile Ala Ala Ala Val Gly Asn Leu
1 5 10 15
Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala Val Leu Tyr Ile
20 25 30
Lys Lys Glu Phe Asn Leu Glu Ser Asn Pro Ser Val Glu Gly Leu Ile
35 40 45
Val Ala Met Ser Leu Ile Gly Ala Thr Leu Ile Thr Thr Cys Ser Gly
50 55 60
Gly Val Ala Asp Trp Leu Gly Arg Arg Pro Met Leu Ile Leu Ser Ser
65 70 75 80
Ile Leu Tyr Phe Val Gly Ser Leu Val Met Leu Trp Ser Pro Asn Val
85 90 95
Tyr Val Leu Leu Leu Gly Arg Leu Leu Asp Gly Phe Gly Val Gly Leu
100 105 110
Val Val Thr Leu Val Pro Ile Tyr Ile Ser Glu Thr Ala Pro Pro Glu
115 120 125
Ile Arg Gly Leu Leu Asn Thr Leu Pro Gln Phe Thr Gly Ser Gly Gly
130 135 140
Met Phe Leu Ser Tyr Cys Met Val Phe Gly Met Ser Leu Met Pro Ser
145 150 155 160
Pro Ser Trp Arg Leu Met Leu Gly Val Leu Phe Ile Pro Ser Leu Val
165 170 175
Phe Phe Phe Leu Thr Val Phe Phe Leu Pro Glu Ser Pro Arg Trp Leu
180 185 190
Val Ser Lys Gly Arg Met Leu Glu Ala Lys Arg Val Leu Gln Arg Leu
195 200 205
Arg Gly Arg Glu Asp Val Ser Gly Glu Met Ala Leu Leu Val Glu Gly
210 215 220
Leu Gly Ile Gly Gly Glu Thr Thr Ile Glu Glu Tyr Ile Ile Gly Pro
225 230 235 240
Ala Asp Glu Val Thr Asp Asp His Asp Ile Ala Val Asp Lys Asp Gln
245 250 255
Ile Lys Leu Tyr Gly Ala Glu Glu Gly Leu Ser Trp Val Ala Arg Pro
260 265 270

BB-1163 US DIV Correct Sequence Listing

Val Lys Gly Gly Ser Thr Met Ser Val Leu Ser Arg His Gly Ser Thr
 275 280 285
 Met Ser Arg Arg Gln Gly Ser Leu Ile Asp Pro Leu Val Thr Leu Phe
 290 295 300
 Gly Ser Val His Glu Lys Met Pro Asp Thr Gly Ser Met Arg Ser Ala
 305 310 315 320
 Leu Phe Pro His Phe Gly Ser Met Phe Ser Val Gly Gly Asn Gln Pro
 325 330 335
 Arg His Glu Asp Trp Asp Glu Glu Asn Leu Val Gly Glu Gly Glu Asp
 340 345 350
 Tyr Pro Ser Asp His Gly Asp Asp Ser Glu Asp Asp Leu His Ser Pro
 355 360 365
 Leu Ile Ser Arg Gln Thr Thr Ser Met Glu Lys Asp Met Pro His Thr
 370 375 380
 Ala His Gly Thr Leu Ser Thr Phe Arg His Gly Ser Gln Val Gln Gly
 385 390 395 400
 Ala Gln Gly Glu Gly Ala Gly Ser Met Gly Ile Gly Gly Gly Trp Gln
 405 410 415
 Val Ala Trp Lys Trp Thr Glu Arg Glu Asp Glu Ser Gly Gln Lys Glu
 420 425 430
 Glu Gly Phe Pro Gly Ser Arg Arg Gly Ser Ile Val Ser Leu Pro Gly
 435 440 445
 Gly Asp Gly Thr Gly Glu Ala Asp Phe Val Gln Ala Ser Ala Leu Val
 450 455 460
 Ser Gln Pro Ala Leu Tyr Ser Lys Asp Leu Leu Lys Glu His Thr Ile
 465 470 475 480
 Gly Pro Ala Met Val His Pro Ser Glu Thr Thr Lys Gly Ser Ile Trp
 485 490 495
 His Asp Leu His Asp Pro Gly Val Lys Arg Ala Leu Val Val Gly Val
 500 505 510
 Gly Leu Gln Ile Leu Gln Gln Phe Ser Gly Ile Asn Gly Val Leu Tyr
 515 520 525
 Tyr Thr Pro Gln Ile Leu Glu Gln Ala Gly Val Gly Ile Leu Leu Ser
 530 535 540
 Asn Met Gly Ile Ser Ser Ser Ser Ala Ser Leu Leu Ile Ser Ala Leu
 545 550 555 560
 Thr Thr Phe Val Met Leu Pro Ala Ile Ala Val Ala Met Arg Leu Met
 565 570 575
 Asp Leu Ser Gly Arg Arg Thr Leu Leu Leu Thr Thr Ile Pro Ile Leu
 580 585 590
 Ile Ala Ser Leu Leu Val Leu Val Ile Ser Asn Leu Val His Met Asn
 595 600 605

BB-1163 US DIV Correct Sequence Listing

Ser Ile Val His Ala Val Leu Ser Thr Val Ser Val Val Leu Tyr Phe
610 615 620
Cys Phe Phe Val Met Gly Phe Gly Pro Ala Pro Asn Ile Leu Cys Ser
625 630 635 640
Glu Ile Phe Pro Thr Arg Val Arg Gly Ile Cys Ile Ala Ile Cys Ala
645 650 655
Leu Thr Phe Trp Ile Cys Asp Ile Ile Val Thr Tyr Ser Leu Pro Val
660 665 670
Leu Leu Lys Ser Ile Gly Leu Ala Gly Val Phe Gly Met Tyr Ala Ile
675 680 685
Val Cys Cys Ile Ser Trp Val Phe Val Phe Ile Lys Val Pro Glu Thr
690 695 700
Lys Gly Met Pro Leu Glu Val Ile Thr Glu Phe Phe Ser Val Gly Ala
705 710 715 720
Arg Gln Ala Glu Ala Ala Lys Asn Glu
725

<210> 30
<211> 549
<212> PRT
<213> Beta vulgaris

<400> 30
Met Ser Glu Gly Thr Asn Lys Ala Met Ser Asp Pro Pro Pro Thr Thr
1 5 10 15
Ala Ser Lys Val Ile Ala Asp Phe Asp Pro Leu Lys Lys Pro Pro Lys
20 25 30
Arg Asn Lys Phe Ala Phe Ala Cys Ala Thr Leu Ala Ser Met Thr Ser
35 40 45
Val Leu Leu Gly Tyr Asp Ile Gly Val Met Ser Gly Ala Ile Ile Tyr
50 55 60
Leu Lys Glu Asp Trp His Ile Ser Asp Thr Gln Ile Gly Val Leu Val
65 70 75 80
Gly Ile Leu Asn Ile Tyr Cys Leu Phe Gly Ser Phe Ala Ala Gly Arg
85 90 95
Thr Ser Asp Trp Ile Gly Arg Arg Tyr Thr Ile Val Leu Ala Gly Ala
100 105 110
Ile Phe Phe Val Gly Ala Leu Leu Met Gly Phe Ala Thr Asn Tyr Ala
115 120 125
Phe Leu Met Val Gly Arg Phe Val Thr Gly Ile Gly Val Gly Tyr Ala
130 135 140
Leu Met Ile Ala Pro Val Tyr Thr Ala Glu Val Ser Pro Ala Ser Ser
145 150 155 160
Arg Gly Phe Leu Thr Ser Phe Pro Glu Val Phe Ile Asn Ala Gly Ile
165 170 175

BB-1163 US DIV Correct Sequence Listing

Leu Leu Gly Tyr Ile Ser Asn Leu Ala Phe Ser Ser Leu Pro Thr His
 180 185 190
 Leu Ser Trp Arg Phe Met Leu Gly Ile Gly Ala Ile Pro Ser Ile Phe
 195 200 205
 Leu Ala Ile Gly Val Leu Ala Met Pro Glu Ser Pro Arg Trp Leu Val
 210 215 220
 Met Gln Gly Arg Leu Gly Asp Ala Lys Lys Val Leu Asn Arg Ile Ser
 225 230 235 240
 Asp Ser Pro Glu Glu Ala Gln Leu Arg Leu Ser Glu Ile Lys Gln Thr
 245 250 255
 Ala Gly Ile Pro Ala Glu Cys Asp Glu Asp Ile Tyr Lys Val Glu Lys
 260 265 270
 Thr Lys Ile Lys Ser Gly Asn Ala Val Trp Lys Glu Leu Phe Phe Asn
 275 280 285
 Pro Thr Pro Ala Val Arg Arg Ala Val Ile Ala Gly Ile Gly Ile His
 290 295 300
 Phe Phe Gln Gln Ala Ser Gly Ile Asp Ala Val Val Leu Tyr Ser Pro
 305 310 315 320
 Arg Ile Phe Gln Ser Ala Gly Ile Thr Asn Ala Arg Lys Gln Leu Leu
 325 330 335
 Ala Thr Val Ala Val Gly Val Val Lys Thr Leu Phe Ile Leu Val Ala
 340 345 350
 Thr Phe Gln Leu Asp Lys Tyr Gly Arg Arg Pro Leu Leu Leu Thr Ser
 355 360 365
 Val Gly Gly Met Ile Ile Ala Ile Leu Thr Leu Ala Met Ser Leu Thr
 370 375 380
 Val Ile Asp His Ser His His Lys Ile Thr Trp Ala Ile Ala Leu Cys
 385 390 395 400
 Ile Thr Met Val Cys Ala Val Val Ala Ser Phe Ser Ile Gly Leu Gly
 405 410 415
 Pro Ile Thr Trp Val Tyr Ser Ser Glu Val Phe Pro Leu Arg Leu Arg
 420 425 430
 Ala Gln Gly Thr Ser Met Gly Val Ala Val Asn Arg Val Val Ser Gly
 435 440 445
 Val Ile Ser Ile Phe Phe Leu Pro Leu Ser His Lys Ile Thr Thr Gly
 450 455 460
 Gly Ala Phe Phe Leu Phe Gly Gly Ile Ala Ile Ile Ala Trp Phe Phe
 465 470 475 480
 Phe Leu Thr Phe Leu Pro Glu Thr Arg Gly Arg Thr Leu Glu Asn Met
 485 490 495
 His Glu Leu Phe Glu Asp Phe Arg Trp Arg Glu Ser Phe Pro Gly Asn
 500 505 510

BB-1163 US DIV Correct Sequence Listing

Lys Ser Asn Asn Asp Glu Asn Ser Thr Arg Lys Gln Ser Asn Gly Asn
515 520 525

Asp Lys Ser Gln Val Gln Leu Gly Glu Thr Thr Thr Ser Thr Thr Val
530 535 540

Thr Asn Asp Asn His
545